

## SEQUENCE LISTING

<110> YAMAMOTO, SACHIKO  
HANADA, TOSHIRO  
SHIRO, MINORU  
KOBATAKE, SHINZO

<120> HYBRID ENZYMES AND USE THEREOF

<130> 55986(70281)

<140> 09/879,257

<141> 2001-06-12

<160> 56

<170> PatentIn Ver. 2.1

<210> 1

<211> 206

<212> PRT

<213> Homo sapiens

<400> 1

Gln Thr Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu Ser Asp  
1 5 10 15

Thr Ser Tyr Val Ser Leu Lys Ala Pro Leu Thr Lys Pro Leu Lys Ala  
20 25 30

Phe Thr Val Cys Leu His Phe Tyr Thr Glu Leu Ser Ser Thr Arg Gly  
35 40 45

Tyr Ser Ile Phe Ser Tyr Ala Thr Lys Arg Gln Asp Asn Glu Ile Leu  
50 55 60

Ile Phe Trp Ser Lys Asp Ile Gly Tyr Ser Phe Thr Val Gly Gly Ser  
65 70 75 80

Glu Ile Leu Phe Glu Val Pro Glu Val Thr Val Ala Pro Val His Ile  
85 90 95

Cys Thr Ser Trp Glu Ser Ala Ser Gly Ile Val Glu Phe Trp Val Asp  
100 105 110

Gly Lys Pro Arg Val Arg Lys Ser Leu Lys Lys Gly Tyr Thr Val Gly  
115 120 125

Ala Glu Ala Ser Ile Ile Leu Gly Gln Glu Gln Asp Ser Phe Gly Gly  
130 135 140

Asn Phe Glu Gly Ser Gln Ser Leu Val Gly Asp Ile Gly Asn Val Asn  
145 150 155 160

Met Trp Asp Phe Val Leu Ser Pro Asp Glu Ile Asn Thr Ile Tyr Leu  
165 170 175

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Gly Gly Pro Phe Ser Pro Asn Val Leu Asn Trp Arg Ala Leu Lys Tyr  
                     180                    185                    190

Glu Val Gln Gly Glu Val Phe Thr Lys Pro Gln Leu Trp Pro  
                     195                    200                    205

<210> 2  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu Ser Asp Thr Ser  
       1                    5                    10                    15

<210> 3  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Leu Val Gly Asp Ile Gly Asn Val Asn Met Trp Asp Phe Val Leu Ser  
       1                    5                    10                    15

Pro Asp Glu Ile Asn Thr Ile Tyr Leu Gly Gly  
                     20                    25

<210> 4  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Leu Lys Lys Gly Tyr Thr Val Gly Ala Glu Ala Ser  
       1                    5                    10

<210> 5  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Arg Ala Leu Lys Tyr Glu Val Gln Gly Glu  
       1                    5                    10

<210> 6  
 <211> 486  
 <212> PRT  
 <213> Leuconostoc mesenteroides

<400> 6  
 Met Val Ser Glu Ile Lys Thr Leu Val Thr Phe Phe Gly Gly Thr Gly  
       1                    5                    10                    15

Asp Leu Ala Lys Arg Lys Leu Tyr Pro Ser Val Phe Asn Leu Tyr Lys  
                   20                  25                  30  
 Lys Gly Tyr Leu Gln Lys His Phe Ala Ile Val Gly Thr Ala Arg Gln  
                   35                  40                  45  
 Ala Leu Asn Asp Asp Glu Phe Lys Gln Leu Val Arg Asp Ser Ile Lys  
                   50                  55                  60  
 Asp Phe Thr Asp Asp Gln Ala Gln Ala Glu Ala Phe Ile Glu His Phe  
                   65                  70                  75                  80  
 Ser Tyr Arg Ala His Asp Val Thr Asp Ala Ala Ser Tyr Ala Val Leu  
                   85                  90                  95  
 Lys Glu Ala Ile Glu Glu Ala Ala Asp Lys Phe Asp Ile Asp Gly Asn  
                   100                  105                  110  
 Arg Ile Phe Tyr Met Ser Val Ala Pro Arg Phe Phe Gly Thr Ile Ala  
                   115                  120                  125  
 Lys Tyr Leu Lys Ser Glu Gly Leu Leu Ala Asp Thr Gly Tyr Asn Arg  
                   130                  135                  140  
 Leu Met Ile Glu Lys Pro Phe Gly Thr Ser Tyr Asp Thr Ala Ala Glu  
                   145                  150                  155                  160  
 Leu Gln Asn Asp Leu Glu Asn Ala Phe Asp Asp Asn Gln Leu Phe Arg  
                   165                  170                  175  
 Ile Asp His Tyr Leu Gly Lys Glu Met Val Gln Asn Ile Ala Ala Leu  
                   180                  185                  190  
 Arg Phe Gly Asn Pro Ile Phe Asp Ala Ala Trp Asn Lys Asp Tyr Ile  
                   195                  200                  205  
 Lys Asn Val Gln Val Thr Leu Ser Glu Val Leu Gly Val Glu Glu Arg  
                   210                  215                  220  
 Ala Gly Tyr Tyr Asp Thr Ala Gly Ala Leu Leu Asp Met Ile Gln Asn  
                   225                  230                  235                  240  
 His Thr Met Gln Ile Val Gly Trp Leu Ala Met Glu Lys Pro Glu Ser  
                   245                  250                  255  
 Phe Thr Asp Lys Asp Ile Arg Ala Ala Lys Asn Ala Ala Phe Asn Ala  
                   260                  265                  270  
 Leu Lys Ile Tyr Asp Glu Ala Glu Val Asn Lys Tyr Phe Val Arg Ala  
                   275                  280                  285  
 Gln Tyr Gly Ala Gly Asp Ser Ala Asp Phe Lys Pro Tyr Leu Glu Glu  
                   290                  295                  300  
 Leu Asp Val Pro Ala Asp Ser Lys Asn Asn Thr Phe Ile Ala Gly Glu  
                   305                  310                  315                  320

Leu Gln Phe Asp Leu Pro Arg Trp Glu Gly Val Pro Phe Tyr Val Arg  
                             325                            330                            335  
 Ser Gly Lys Arg Leu Ala Ala Lys Gln Thr Arg Val Asp Ile Val Phe  
                             340                            345                            350  
 Lys Ala Gly Thr Phe Asn Phe Gly Ser Glu Gln Glu Ala Gln Glu Ala  
                             355                            360                            365  
 Val Leu Ser Ile Ile Ile Asp Pro Lys Gly Ala Ile Glu Leu Lys Leu  
                             370                            375                            380  
 Asn Ala Lys Ser Val Glu Asp Ala Phe Asn Thr Arg Thr Ile Asp Leu  
                             385                            390                            395                            400  
 Gly Trp Thr Val Ser Asp Glu Asp Lys Lys Asn Thr Pro Glu Pro Tyr  
                             405                            410                            415  
 Glu Arg Met Ile His Asp Thr Met Asn Gly Asp Gly Ser Asn Phe Ala  
                             420                            425                            430  
 Asp Trp Asn Gly Val Ser Ile Ala Trp Lys Phe Val Asp Ala Ile Ser  
                             435                            440                            445  
 Ala Val Tyr Thr Ala Asp Lys Ala Pro Leu Glu Thr Tyr Lys Ser Gly  
                             450                            455                            460  
 Ser Met Gly Pro Glu Ala Ser Asp Lys Leu Leu Ala Ala Asn Gly Asp  
                             465                            470                            475                            480  
 Ala Trp Val Phe Lys Gly  
                             485

<210> 7  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 ataaggggta caccatgggtt tcagaaatca agacgtag

39

<210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 ttcccggtt ttaattaacc tttaaacc

30

<210> 9  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9  
 tggttggtta gctatggaaa aaccagaatc

30

<210> 10  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10  
 taggatccag gtacgtctaa ttcttcaagg tatg

34

<210> 11  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11  
 atggatccgc tgattctaaa aacaatacct tc

32

<210> 12  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12  
 aagcttgcat gcctgcaggt tcccg

25

<210> 13  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 2, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 13  
 gatccgacat gtcgaggaag gcttttgtgt ttcccaaaga gtcggatact tccg 54

<210> 14  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 14  
 gatccggaag tatccgactc tttgggaaac acaaaagcct tcctcgacat gtcg 54

<210> 15  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 3, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 15  
 gatccgtgct gtcaccagat gagattaaca ccattctatct tggcgggg 48

<210> 16  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 16  
 gatccccgc caagatagat ggtgttaatc tcattctggtg acagcacg 48

<210> 17  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 4, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 17  
 gatccctgaa gaagggatac actgtggggg cagaagcaag cg 42

<210> 18  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 18  
 gatccgcttg cttctgcccc cacagtgtat cccttcttca gg 42

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 5, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 19  
 gatcccgggc actgaagtat gaagtgcaag gcgaag 36

<210> 20  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 20  
 gatccttcgc cttgcacttc atacttcagt gcccg 36

<210> 21  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 3, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 21  
 gatcctagtg ggagacattg gaaatgtgaa catgtgggac tttgtgg 47

<210> 22  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 22  
 gatcccacaa agtcccacat gttcacattt ccaatgtctc ccactag 47

<210> 23  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 23  
 taggatccgt ctaattcttc aaggatggc ttg 33

<210> 24  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 24  
 aaggatccgt acctgctgat tctaaaaaca atac 34

<210> 25  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 25  
 ttgatccag caggtacgtc taattcttca ag 32

<210> 26  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Primer

<400> 26

taggatccga ttctaaaaac aataccttca tcg 33

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27

gggtgtttaa aggtggatcc taattaaagc ccgg 34

<210> 28

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28

taggatcctt ctgaacccaa gttaaactg cc 32

<210> 29

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

atggatccca agaagcacia gaagctgtct tg 32

<210> 30

<211> 1024

<212> PRT

<213> Escherichia coli

<400> 30

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp  
1 5 10 15

Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro  
20 25 30

Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro  
35 40 45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe  
 50 55 60  
 Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro  
 65 70 75 80  
 Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr  
 85 90 95  
 Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro  
 100 105 110  
 Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe  
 115 120 125  
 Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe  
 130 135 140  
 Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val  
 145 150 155 160  
 Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala  
 165 170 175  
 Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp  
 180 185 190  
 Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly  
 195 200 205  
 Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser  
 210 215 220  
 Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val  
 225 230 235 240  
 Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg  
 245 250 255  
 Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr  
 260 265 270  
 Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly Gly Tyr Ala Asp  
 275 280 285  
 Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala  
 290 295 300  
 Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp  
 305 310 315 320  
 Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val  
 325 330 335  
 Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile  
 340 345 350

Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met	355	360	365
Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn	370	375	380
Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr	385	390	395
Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile	405	410	415
Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg	420	425	430
Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp	435	440	445
Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly	450	455	460
His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp	465	470	475
Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala	485	490	495
Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro	500	505	510
Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro	515	520	525
Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly	530	535	540
Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr	545	550	555
Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu	565	570	575
Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp	580	585	590
Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val	595	600	605
Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln	610	615	620
Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr	625	630	635
Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met	645	650	655

Val	Ala	Leu	Asp	Gly	Lys	Pro	Leu	Ala	Ser	Gly	Glu	Val	Pro	Leu	Asp	660	665	670	
Val	Ala	Pro	Gln	Gly	Lys	Gln	Leu	Ile	Glu	Leu	Pro	Glu	Leu	Pro	Gln	675	680	685	
Pro	Glu	Ser	Ala	Gly	Gln	Leu	Trp	Leu	Thr	Val	Arg	Val	Val	Gln	Pro	690	695	700	
Asn	Ala	Thr	Ala	Trp	Ser	Glu	Ala	Gly	His	Ile	Ser	Ala	Trp	Gln	Gln	705	710	715	720
Trp	Arg	Leu	Ala	Glu	Asn	Leu	Ser	Val	Thr	Leu	Pro	Ala	Ala	Ser	His	725	730	735	
Ala	Ile	Pro	His	Leu	Thr	Thr	Ser	Glu	Met	Asp	Phe	Cys	Ile	Glu	Leu	740	745	750	
Gly	Asn	Lys	Arg	Trp	Gln	Phe	Asn	Arg	Gln	Ser	Gly	Phe	Leu	Ser	Gln	755	760	765	
Met	Trp	Ile	Gly	Asp	Lys	Lys	Gln	Leu	Leu	Thr	Pro	Leu	Arg	Asp	Gln	770	775	780	
Phe	Thr	Arg	Ala	Pro	Leu	Asp	Asn	Asp	Ile	Gly	Val	Ser	Glu	Ala	Thr	785	790	795	800
Arg	Ile	Asp	Pro	Asn	Ala	Trp	Val	Glu	Arg	Trp	Lys	Ala	Ala	Gly	His	805	810	815	
Tyr	Gln	Ala	Glu	Ala	Ala	Leu	Leu	Gln	Cys	Thr	Ala	Asp	Thr	Leu	Ala	820	825	830	
Asp	Ala	Val	Leu	Ile	Thr	Thr	Ala	His	Ala	Trp	Gln	His	Gln	Gly	Lys	835	840	845	
Thr	Leu	Phe	Ile	Ser	Arg	Lys	Thr	Tyr	Arg	Ile	Asp	Gly	Ser	Gly	Gln	850	855	860	
Met	Ala	Ile	Thr	Val	Asp	Val	Glu	Val	Ala	Ser	Asp	Thr	Pro	His	Pro	865	870	875	880
Ala	Arg	Ile	Gly	Leu	Asn	Cys	Gln	Leu	Ala	Gln	Val	Ala	Glu	Arg	Val	885	890	895	
Asn	Trp	Leu	Gly	Leu	Gly	Pro	Gln	Glu	Asn	Tyr	Pro	Asp	Arg	Leu	Thr	900	905	910	
Ala	Ala	Cys	Phe	Asp	Arg	Trp	Asp	Leu	Pro	Leu	Ser	Asp	Met	Tyr	Thr	915	920	925	
Pro	Tyr	Val	Phe	Pro	Ser	Glu	Asn	Gly	Leu	Arg	Cys	Gly	Thr	Arg	Glu	930	935	940	
Leu	Asn	Tyr	Gly	Pro	His	Gln	Trp	Arg	Gly	Asp	Phe	Gln	Phe	Asn	Ile	945	950	955	960

Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu  
                                   965                                  970                                  975

Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met  
                                   980                                  985                                  990

Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe  
                                   995                                  1000                                  1005

Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln Lys  
           1010                                  1015                                  1020

<210> 31

<211> 448

<212> PRT

<213> Escherichia coli

<400> 31

Thr Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile  
   1                                  5                                  10                                  15

Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala  
                                   20                                  25                                  30

Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu  
                                   35                                  40                                  45

Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr  
   50                                  55                                  60

Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu  
   65                                  70                                  75                                  80

Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro  
                                   85                                  90                                  95

Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly  
                                   100                                  105                                  110

Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp  
                                   115                                  120                                  125

His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly  
   130                                  135                                  140

Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val  
   145                                  150                                  155                                  160

Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu  
                                   165                                  170                                  175

Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr  
                                   180                                  185                                  190

Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	Leu	Gly	Gly	Gly	Ala	195	200	205
Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	Glu	Trp	Gln	Gly	Lys	Thr	210	215	220
Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	Gln	Leu	Val	Ser	Asp	Ala	225	230	235
Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	Gln	Gln	Lys	Pro	Leu	Leu	245	250	255
Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	Arg	Trp	Leu	Gly	Pro	Lys	260	265	270
Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys	Thr	Pro	275	280	285
Asn	Pro	Gln	Arg	Asn	Asp	Ser	Val	Pro	Thr	Leu	Ala	Gln	Met	Thr	Asp	290	295	300
Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	Lys	Gly	Phe	Phe	Leu	Gln	305	310	315
Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	His	Ala	Ala	Asn	Pro	Cys	325	330	335
Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	Glu	Ala	Val	Gln	Arg	Ala	340	345	350
Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	Leu	Val	Ile	Val	Thr	Ala	355	360	365
Asp	His	Ala	His	Ala	Ser	Gln	Ile	Val	Ala	Pro	Asp	Thr	Lys	Ala	Pro	370	375	380
Gly	Leu	Thr	Gln	Ala	Leu	Asn	Thr	Lys	Asp	Gly	Ala	Val	Met	Val	Met	385	390	395
Ser	Tyr	Gly	Asn	Ser	Glu	Glu	Asp	Ser	Gln	Glu	His	Thr	Gly	Gln	Leu	405	410	415
Arg	Ile	Ala	Ala	Tyr	Gly	Pro	His	Ala	Ala	Asn	Val	Val	Gly	Leu	Thr	420	425	430
Asp	Gln	Thr	Asp	Leu	Phe	Tyr	Thr	Met	Lys	Ala	Ala	Leu	Gly	Leu	Lys	435	440	445

&lt;210&gt; 32

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide consisting of DNA coding for amino acids of Sequence 2, and a partial restriction site of BamHI consisting of 5' end of "gatcc" and 3' end of "g"

<400> 32

gatccgacat gtcgaggaag gcttttgtgt ttcccaaaga gtcgg

45

<210> 33

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 33

gatcccgact ctttgggaaa cacaaaagcc ttctcgaca tgtcg

45

<210> 34

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide consisting of DNA coding for amino acids of Sequence 2, and a partial restriction site of BamHI consisting of 5' end of "gatcc" and 3' end of "g"

<400> 34

gatccaggaa ggcttttgtg tttcccaaag agtcgg

36

<210> 35

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35

gatcccgact ctttgggaaa cacaaaagcc ttctg

36

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

cacaggaaac agaccatggg atccgtttca gaaatc

36

<210> 37

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

ttggatccat caccggcacc atattgtgca cg

32

<210> 38

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

aaggatcctc agctgacttc aagccatacc ttg

33

<210> 39

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

aaggatccaa ggtatggctt gaagtcagct g

31

<210> 40

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

aaggatccaa ggtatggctt gaagtcagct g

31

<210> 41

<211> 30



<212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41

ggtacgtata attcatcaag gtatggcttg

30

<210> 42

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 42

tatacgtacc tgctgattct aaaaac

26

<210> 43

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for  
 amino acids of Sequence 2

<400> 43

aggaaggctt ttgtgtttcc caaagagtcg

30

<210> 44

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 44

cgactctttg ggaaacacaa aagccttcct

30

<210> 45

<211> 55

<212> PRT

<213> Hepatitis B Virus

<400> 45

Met Gln Trp Asn Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg  
 1 5 10 15

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
                   20                  25                  30

Asn Pro Ala Pro Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg  
           35                  40                  45

Thr Gly Asp Pro Val Thr Asn  
       50                  55

<210> 46

<211> 12

<212> PRT

<213> Hepatitis B Virus

<400> 46

Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly  
       1                  5                  10

<210> 47

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
       oligonucleotide consisting of DNA coding for amino acids  
       of Sequence 46, and a partial restriction site of BamHI  
       consisting of 5' end of "gatcc" and 3' end of "g"

<400> 47

gatccgaccc gcgtgttcgt ggtctgtatt tcccggctgg tg 42

<210> 48

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
       oligonucleotide

<400> 48

gatccaccag ccgggaaata cagaccacga acacgcgggt cc 42

<210> 49

<211> 84

<212> PRT

<213> Homo sapiens

<400> 49

Ala Val Ser Glu Ile Gln Phe Met His Asn Leu Gly Lys His Leu Ser  
       1                  5                  10                  15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His  
                   20                  25                  30

Asn Phe Val Ala Leu Gly Ala Ser Ile Ala Tyr Arg Asp Gly Ser Ser  
                   35                  40                  45

Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His Gln  
                   50                  55                  60

Lys Ser Leu Gly Glu Ala Asp Lys Ala Asp Val Asp Val Leu Ile Lys  
                   65                  70                  75                  80

Ala Lys Pro Gln

<210> 50  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His Asn  
           1                  5                  10                  15

<210> 51  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide consisting of DNA coding for amino acids  
 of Sequence 50, and a partial restriction site of BamHI  
 consisting of 5' end of "gatcc" and 3' end of "g"

<400> 51  
 gatccgaacg tggtgaatgg ctgcgtaaaa aactgcagga cgttcataac g 51

<210> 52  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 52  
 gatccggttat gaacgtcctg cagtttttta cgcagccatt caacacgttc g 51

<210> 53  
 <211> 28

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 53  
 tatgaccatg attacggatt cactggcc 28

<210> 54  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 54  
 ctgcccggtt attattattt ttgacaccag 30

<210> 55  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 55  
 taggatccta cgccaatgtc gttatccagc g 31

<210> 56  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 56  
 ttggatccag tgaagcgacc cgcattgacc 30